

## SEQUENCE LISTING

<110> Moore, Paul A.  
Rosen, Craig A.  
Ruben, Steven M.

<120> Cytokine Receptor Common Gamma Chain Like

<130> PF466P1

<140> Unassigned

<141> 1999-08-18

<150> 60/086,505

<151> 1998-05-22

<150> 60/078,563

<151> 1998-03-19

<150> 09/263,626

<151> 1999-03-05

<150> PCT/US99/05068

<151> 1999-03-05

<160> 32

<170> PatentIn Ver. 2.0

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ctg ctg gga ggc tgg atg gct ttg ggg caa gga gga gca gca gaa gga 99  
Leu Leu Gly Gly Trp Met Ala Leu Gly Gln Gly Gly Ala Ala Glu Gly  
15 20 25

gta cag att cag atc atc tac ttc aat tta gaa acc gtg cag gtg aca 147  
Val Gln Ile Gln Ile Ile Tyr Phe Asn Leu Glu Thr Val Gln Val Thr  
30 35 40 45

tgg aat gcc agc aaa tac tcc agg acc aac ctg act ttc cac tac aga 195  
Trp Asn Ala Ser Lys Tyr Ser Arg Thr Asn Leu Thr Phe His Tyr Arg  
50 55 60

ttc aac ggt gat gag gcc tat gac cag tgc acc aac tac ctt ctc cag 243  
Phe Asn Gly Asp Glu Ala Tyr Asp Gln Cys Thr Asn Tyr Leu Leu Gln  
65 70 75

gaa ggt cac act tcg ggg tgc ctc cta gac gca gag cag cga gac gac 291  
Glu Gly His Thr Ser Gly Cys Leu Leu Asp Ala Glu Gln Arg Asp Asp  
80 85 90



att ctc tat ttc tcc atc agg aat ggg acg cac ccc gtt ttc acc gca Ile Leu Tyr Phe Ser Ile Arg Asn Gly Thr His Pro Val Phe Thr Ala 95 100 105	339
agt cgc tgg atg gtt tat tac ctg aaa ccc agt tcc ccg aag cac gtg Ser Arg Trp Met Val Tyr Tyr Leu Lys Pro Ser Ser Pro Lys His Val 110 115 120 125	387
aga ttt tcg tgg cat cag gat gca gtg acg gtg acg tgt tct gac ctg Arg Phe Ser Trp His Gln Asp Ala Val Thr Val Thr Cys Ser Asp Leu 130 135 140	435
tcc tac ggg gat ctc ctc tat gag gtt cag tac cgg agc ccc ttc gac Ser Tyr Gly Asp Leu Leu Tyr Glu Val Gln Tyr Arg Ser Pro Phe Asp 145 150 155	483
acc gag tgg cag tcc aaa cag gaa aat acc tgc aac gtc acc ata gaa Thr Glu Trp Gln Ser Lys Gln Glu Asn Thr Cys Asn Val Thr Ile Glu 160 165 170	531
ggc ttg gat gcc gag aag tgt tac tct ttc tgg gtc agg gtg aag gct Gly Leu Asp Ala Glu Lys Cys Tyr Ser Phe Trp Val Arg Val Lys Ala 175 180 185	579
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cca acg cct ccc aaa cca aag ctg tcc aaa ttt att tta att tcc agc Pro Thr Pro Pro Lys Pro Lys Leu Ser Lys Phe Ile Leu Ile Ser Ser 225 230 235	723
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tcc atc ttc ccc ggg ctc ttt gag ata cac caa ggg aac ttc cag gag Ser Ile Phe Pro Gly Leu Phe Glu Ile His Gln Gly Asn Phe Gln Glu 270 275 280 285	867
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cgc tcc tac gtg gcg ttg tgatggacac accactgtca aagtcaacgt 1155  
 Arg Ser Tyr Val Ala Leu  
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 Asp Glu Ala Tyr Asp Gln Cys Thr Asn Tyr Leu Leu Gln Glu Gly His  
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 Thr Ser Gly Cys Leu Leu Asp Ala Glu Gln Arg Asp Asp Ile Leu Tyr  
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 Met Val Tyr Tyr Leu Lys Pro Ser Ser Pro Lys His Val Arg Phe Ser  
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 Trp His Gln Asp Ala Val Thr Val Thr Cys Ser Asp Leu Ser Tyr Gly  
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 Asp Leu Leu Tyr Glu Val Gln Tyr Arg Ser Pro Phe Asp Thr Glu Trp  
 145 150 155 160  
 Gln Ser Lys Gln Glu Asn Thr Cys Asn Val Thr Ile Glu Gly Leu Asp  
 165 170 175

Ala Glu Lys Cys Tyr Ser Phe Trp Val Arg Val Lys Ala Met Glu Asp  
 180 185 190

Val Tyr Gly Pro Asp Thr Tyr Pro Ser Asp Trp Ser Glu Val Thr Cys  
 195 200 205

Trp Gln Arg Gly Glu Ile Arg Asp Ala Cys Ala Glu Thr Pro Thr Pro  
 210 215 220

Pro Lys Pro Lys Leu Ser Lys Phe Ile Leu Ile Ser Ser Leu Ala Ile  
 225 230 235 240

Leu Leu Met Val Ser Leu Leu Leu Leu Ser Leu Trp Lys Leu Trp Arg  
 245 250 255

Val Lys Lys Phe Leu Ile Pro Ser Val Pro Asp Pro Lys Ser Ile Phe  
 260 265 270

Pro Gly Leu Phe Glu Ile His Gln Gly Asn Phe Gln Glu Trp Ile Thr  
 275 280 285

Asp Thr Gln Asn Val Ala His Leu His Lys Met Ala Gly Ala Glu Gln  
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Glu Ser Gly Pro Glu Glu Pro Leu Val Val Gln Leu Ala Lys Thr Glu  
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Ala Glu Ser Pro Arg Met Leu Asp Pro Gln Thr Glu Glu Lys Glu Ala  
 325 330 335

Ser Gly Gly Ser Leu Gln Leu Pro His Gln Pro Leu Gln Gly Gly Asp  
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Thr Ser Thr Pro Ala Gly Thr Leu Asp Val Ser Thr Leu Pro Leu Pro  
 35 40 45

Lys Val Gln Cys Phe Val Phe Asn Val Glu Tyr Met Asn Cys Thr Trp  
 50 55 60

Asn Ser Ser Ser Glu Pro Gln Pro Asn Asn Leu Thr Leu His Tyr Gly  
 65 70 75 80

Tyr Arg Asn Phe Asn Gly Asp Asp Lys Leu Gln Glu Cys Gly His Tyr  
 85 90 95

Leu Phe Ser Glu Gly Ile Thr Ser Gly Cys Trp Phe Gly Lys Lys Glu  
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 Ile Arg Leu Tyr Glu Thr Phe Val Val Gln Leu Gln Asp Pro Arg Glu  
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 His Arg Lys Gln Pro Lys Gln Met Leu Lys Leu Gln Asp Leu Val Ile  
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 Pro Trp Ala Pro Glu Asn Leu Thr Leu Arg Asn Leu Ser Glu Phe Gln  
 145 150 155 160  
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 165 170 175  
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 180 185 190  
 Val Asp His Arg His Ser Phe Ser Leu Pro Ser Val Asp Ala Gln Lys  
 195 200 205  
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 210 215 220  
 Ala Gln His Trp Ser Asp Trp Ser Tyr Pro Ile His Trp Gly Ser Asn  
 225 230 235 240  
 Thr Ser Lys Glu Asn Ile Glu Asn Pro Glu Asn Pro Ser Leu Phe Ala  
 245 250 255  
 Leu Glu Ala Val Leu Ile Pro Leu Gly Ser Met Gly Leu Ile Val Ser  
 260 265 270  
 Leu Ile Cys Val Tyr Cys Trp Leu Glu Arg Thr Met Pro Arg Ile Pro  
 275 280 285  
 Thr Leu Lys Asn Leu Glu Asp Leu Val Thr Glu Tyr Gln Gly Asn Phe  
 290 295 300  
 Ser Ala Trp Ser Gly Val Ser Lys Gly Leu Ala Glu Ser Leu Gln Pro  
 305 310 315 320  
 Asp Tyr Ser Glu Arg Leu Cys His Val Ser Glu Ile Pro Pro Lys Gly  
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 ggctgaatgg caaggagtac aagtgaagg tctccaacaa agccctccca acccccatcg 360  
 agaaaacat ctccaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420  
 catcccgga tgagctgacc aagaaccagg tcagcctgac ctgcctgggc aaaggttct 480  
 atccaagcga catcgccgtg gagggggaga gcaatgggca gccggagaac aactacaaga 540  
 ccacgcctcc cgtgctggac tccgacggct ccttcttct ctacagcaag ctccacgtgg 600  
 acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggtctctgc 660  
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 cagttccgcc cattctccgc cccatggctg actaattttt tttatttatg cagaggccga 180  
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 <222> (5)



<223> Xaa equals any amino acid

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 Gly His Thr Ser Gly Cys  
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His Arg Lys Ser Leu Asp Gly Leu Leu Pro Glu Thr Gln Phe  
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Glu Lys Cys Tyr Ser Phe Trp Val Arg Val Lys Ala Met Glu Asp Val  
 35 40 45

Tyr Gly Pro Asp Thr Tyr Pro Ser Asp Trp Ser Glu Val Thr Cys Trp  
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Gln Arg Gly Glu Ile Arg Asp Ala Cys Ala Glu Thr Pro Thr Pro Pro  
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Lys

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 Pro Thr Pro Pro Lys Pro Lys Leu Ser Lys Phe Ile Leu Ile Ser Ser  
           35                  40                  45  
 Leu Ala Ile Leu Leu Met Val Ser Leu Leu Leu Ser Leu Trp Lys  
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Leu Trp Arg Xaa Lys Lys Phe Leu Xaa Pro Ser Val Pro Asp Pro Lys  
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 Ser Ile Phe Pro Gly Leu Phe Xaa Ile His Gln Gly Asn Phe Gln Glu  
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 Trp Ile Thr Asp Thr Gln Asn Val Ala His Leu His Lys Met Ala Gly  
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 Ala Glu Gln Glu Ser Gly Pro Glu Glu Pro Leu Val Val Gln Leu Ala  
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 Lys Thr Glu Ala Glu Ser Pro Arg Met Leu Asp Pro Gln Thr Glu Glu  
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 Lys Glu Ala Ser Gly Gly Ser Leu Gln Leu Pro His Gln Pro Leu Gln  
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<220>  
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 cagtccaaac aggaaaatac ctgcaacgtc accatagaag gcttggtatgc cgagaagtgt 540  
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 Gln Ile Ile Tyr Phe Asn Leu Glu Thr Val Gln Val Thr Trp Asn Ala  
 35 40 45  
 Ser Lys Tyr Ser Arg Thr Asn Leu Thr Phe His Tyr Arg Phe Asn Gly  
 50 55 60  
 Asp Glu Ala Tyr Asp Gln Cys Thr Asn Tyr Leu Leu Gln Glu Gly His  
 65 70 75 80  
 Thr Ser Gly Cys Leu Leu Asp Ala Xaa Gln Arg Asp Asp Ile Leu Tyr  
 85 90 95  
 Phe Ser Ile Arg Asn Gly Thr His Pro Val Phe Thr Ala Ser Arg Trp  
 100 105 110  
 Met Val Tyr Tyr Leu Lys Pro Ser Ser Pro Lys His Val Arg Phe Arg  
 115 120 125  
 Gly Ile Arg Xaa Asp Gly Asp Val Phe Xaa Thr Cys Pro Thr Gly Ile  
 130 135 140

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Pro Asn Arg Lys Ile Pro Ala Thr Ser Pro  
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 gccatcatgg ggcggctggt tctg 144